

SENT
STIC-Biotech/ChemLib

178686

mg

From: Steadman, David (AU1652)
Sent: Monday, February 06, 2006 1:51 PM
To: STIC-Biotech/ChemLib
Subject: 10/729,571 sequence search request

NAME: David Steadman
AU: 1656
Date: 2/6/06
Office: Remsen 2B05
Mailbox: Remsen 3C70

RECEIVED
FEB - 6 2006
(STIC)

Please search the following sequences in commercial databases:

- 1) SEQ ID NO:2 against amino acid databases.
- 2) SEQ ID NO:2 against nucleic acid databases.

Please save results to diskette.

Thank you very much.

David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1656
Protein Crystallography and Recombinant Enzymes
Office: Remsen 2B05
Mailbox: Remsen 3C70
Phone: (571) 272-0942

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 12:05:19 ; Search time 48 Seconds
 (without alignments)
 439.215 Million cell updates/sec

Title: US-10-729-571B-2
 Perfect score: 1315
 Sequence: 1 MKIGVFD SGVGGF SVLKSL FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				Description
	No.	Score	Match	Length	DB	ID			
1	850.5	64.7	3287	1	US-08-477-451-7				Sequence 7, Appli
2	843	64.1	178	1	US-08-477-451-46				Sequence 46, Appl
3	406	30.9	3200	1	US-08-477-451-8				Sequence 8, Appli
4	360	27.4	269	2	US-09-134-001C-3853				Sequence 3853, Ap
5	325	24.7	271	2	US-09-902-540-9954				Sequence 9954, Ap
6	312	23.7	225	2	US-09-107-433-4069				Sequence 4069, Ap
7	312	23.7	264	1	US-08-759-907-2				Sequence 2, Appli
8	312	23.7	264	2	US-09-303-272-2				Sequence 2, Appli
9	309	23.5	264	2	US-09-583-110-2962				Sequence 2962, Ap
10	261	19.8	297	2	US-09-328-352-8041				Sequence 8041, Ap
11	233	17.7	323	2	US-09-252-991A-30565				Sequence 30565, A
12	225	17.1	126	2	US-09-107-532A-5193				Sequence 5193, Ap

13	222.5	16.9	299	2	US-09-543-681A-8299	Sequence 8299, Ap
14	217	16.5	294	2	US-09-489-039A-12157	Sequence 12157, A
15	186	14.1	90	2	US-09-134-000C-6077	Sequence 6077, Ap
16	171	13.0	261	2	US-09-830-230A-397	Sequence 397, App
17	151	11.5	190	2	US-09-134-000C-6075	Sequence 6075, Ap
18	134	10.2	235	2	US-09-830-230A-398	Sequence 398, App
19	128.5	9.8	211	2	US-09-328-352-4995	Sequence 4995, Ap
20	118.5	9.0	244	2	US-09-107-532A-5302	Sequence 5302, Ap
21	101.5	7.7	748	2	US-09-543-681A-6676	Sequence 6676, Ap
22	100.5	7.6	418	1	US-08-305-764C-58	Sequence 58, Appl
23	100.5	7.6	418	1	US-08-305-764C-60	Sequence 60, Appl
24	100.5	7.6	647	1	US-08-305-764C-56	Sequence 56, Appl
25	94	7.1	442	2	US-09-248-796A-18555	Sequence 18555, A
26	92	7.0	286	2	US-09-134-001C-3571	Sequence 3571, Ap
27	91.5	7.0	945	2	US-08-747-562-16	Sequence 16, Appl
28	89	6.8	69	2	US-09-540-236-2656	Sequence 2656, Ap
29	89	6.8	251	2	US-09-710-279-298	Sequence 298, App
30	89	6.8	251	2	US-09-710-279-722	Sequence 722, App
31	88.5	6.7	243	2	US-09-328-352-6952	Sequence 6952, Ap
32	88.5	6.7	624	1	US-08-846-762-96	Sequence 96, Appl
33	87.5	6.7	672	2	US-09-989-981A-4	Sequence 4, Appli
34	87	6.6	277	2	US-09-489-039A-12020	Sequence 12020, A
35	85	6.5	863	2	US-09-710-279-2010	Sequence 2010, Ap
36	85	6.5	876	2	US-09-134-001C-3943	Sequence 3943, Ap
37	83.5	6.3	281	2	US-09-134-001C-5454	Sequence 5454, Ap
38	83.5	6.3	596	2	US-09-489-039A-9470	Sequence 9470, Ap
39	82.5	6.3	279	2	US-09-704-725-8	Sequence 8, Appli
40	82.5	6.3	531	2	US-09-134-001C-3574	Sequence 3574, Ap
41	82.5	6.3	697	2	US-09-830-433A-52	Sequence 52, Appl
42	82	6.2	396	1	US-07-702-771-1	Sequence 1, Appli
43	82	6.2	418	2	US-10-104-047-2420	Sequence 2420, Ap
44	82	6.2	443	1	US-08-935-450-6	Sequence 6, Appli
45	82	6.2	443	2	US-08-952-899-2	Sequence 2, Appli

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OM protein - protein search, using sw model

Run on: February 9, 2006, 12:06:59 ; Search time 17 Seconds
(without alignments)
196.838 Million cell updates/sec

Title: US-10-729-571B-2
Perfect score: 1315
Sequence: 1 MKIGVFD SGVGGFSVLKSL.....FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	357	27.1	286	7	US-11-098-686-11112	Sequence 11112, A
2	332.5	25.3	326	6	US-10-467-657-7224	Sequence 7224, Ap
3	201.5	15.3	269	7	US-11-194-246-328	Sequence 328, App
4	89	6.8	251	6	US-10-793-626-298	Sequence 298, App
5	89	6.8	251	6	US-10-793-626-722	Sequence 722, App
6	85	6.5	863	6	US-10-793-626-2010	Sequence 2010, Ap
7	83.5	6.3	688	7	US-11-098-686-10843	Sequence 10843, A
8	83	6.3	392	6	US-10-957-569-35	Sequence 35, Appl
9	83	6.3	392	7	US-11-097-589-33	Sequence 33, Appl

10	81.5	6.2	508	6	US-10-467-657-6928	Sequence 6928, Ap
11	79.5	6.0	424	6	US-10-793-626-2296	Sequence 2296, Ap
12	77	5.9	534	7	US-11-089-551A-52	Sequence 52, Appl
13	76	5.8	311	7	US-11-098-686-10342	Sequence 10342, A
14	76	5.8	596	6	US-10-453-372-1212	Sequence 1212, Ap
15	76	5.8	600	6	US-10-453-372-1206	Sequence 1206, Ap
16	75.5	5.7	166	7	US-11-176-830-238	Sequence 238, App
17	75.5	5.7	166	7	US-11-176-830-1234	Sequence 1234, Ap
18	75.5	5.7	166	7	US-11-196-067-430	Sequence 430, App
19	75.5	5.7	356	6	US-10-161-408-50	Sequence 50, Appl
20	75.5	5.7	356	7	US-11-082-154A-38	Sequence 38, Appl
21	75	5.7	166	7	US-11-176-830-1191	Sequence 1191, Ap
22	75	5.7	166	7	US-11-196-067-387	Sequence 387, App
23	75	5.7	406	6	US-10-467-657-1048	Sequence 1048, Ap
24	74.5	5.7	166	7	US-11-176-830-992	Sequence 992, App
25	74.5	5.7	426	6	US-10-873-528-34	Sequence 34, Appl
26	74.5	5.7	598	7	US-11-194-246-306	Sequence 306, App
27	74	5.6	484	6	US-10-873-528-38	Sequence 38, Appl
28	73.5	5.6	166	7	US-11-176-830-1061	Sequence 1061, Ap
29	73.5	5.6	166	7	US-11-176-830-1256	Sequence 1256, Ap
30	73.5	5.6	166	7	US-11-176-830-1290	Sequence 1290, Ap
31	73.5	5.6	166	7	US-11-196-067-257	Sequence 257, App
32	73.5	5.6	166	7	US-11-196-067-452	Sequence 452, App
33	73.5	5.6	166	7	US-11-196-067-486	Sequence 486, App
34	73.5	5.6	321	7	US-11-212-443-10	Sequence 10, Appl
35	73	5.6	600	6	US-10-453-372-1204	Sequence 1204, Ap
36	73	5.6	696	6	US-10-131-826A-354	Sequence 354, App
37	73	5.6	696	6	US-10-511-538-231	Sequence 231, App
38	73	5.6	819	6	US-10-453-372-1210	Sequence 1210, Ap
39	73	5.6	832	6	US-10-989-767A-660	Sequence 660, App
40	73	5.6	853	6	US-10-877-346-30	Sequence 30, Appl
41	73	5.6	866	7	US-11-147-047-32	Sequence 32, Appl
42	73	5.6	876	6	US-10-453-372-1202	Sequence 1202, Ap
43	73	5.6	876	6	US-10-453-372-1208	Sequence 1208, Ap
44	72.5	5.5	166	7	US-11-176-830-1205	Sequence 1205, Ap
45	72.5	5.5	166	7	US-11-196-067-401	Sequence 401, App

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OM protein - protein search, using sw model

Run on: February 9, 2006, 11:58:03 ; Search time 253 Seconds
(without alignments)
711.106 Million cell updates/sec

Title: US-10-729-571B-2
Perfect score: 1315
Sequence: 1 MKIGVFD SGVGGFSVLKSL.....FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1315	100.0	255	1	MURI_HELPJ	Q9zlt0 helicobacte	
2	1249	95.0	255	2	Q6VRG6_HELPY	Q6vrg6 helicobacte	
3	1248	94.9	255	1	MURI_HELPY	P56068 helicobacte	
4	1245	94.7	255	2	Q6VRM6_HELPY	Q6vrm6 helicobacte	
5	1238	94.1	255	2	Q6VRQ4_HELPY	Q6vrq4 helicobacte	
6	1235	93.9	255	2	Q6VRJ5_HELPY	Q6vrj5 helicobacte	
7	1229	93.5	255	2	Q75X40_HELPY	Q75x40 helicobacte	
8	1197	91.0	286	2	Q75XF0_HELPY	Q75xf0 helicobacte	
9	1169	88.9	255	2	Q7WUV0_HELAC	Q7wuv0 helicobacte	
10	1151	87.5	255	2	Q7WUU9_HELAC	Q7wu9 helicobacte	
11	1124	85.5	231	2	Q7X5E0_HELPY	Q7x5e0 helicobacte	
12	1101	83.7	231	2	Q7X5D9_HELPY	Q7x5d9 helicobacte	
13	1050	79.8	232	2	Q7X5I7_HELAC	Q7x5i7 helicobacte	
14	1035	78.7	232	2	Q7X5I6_HELAC	Q7x5i6 helicobacte	
15	871	66.2	184	2	Q7X5D8_HELPY	Q7x5d8 helicobacte	

16	825	62.7	166	2	Q8GK50_HELPY	Q8gk50 helicobacte
17	824	62.7	166	2	Q8GJZ0_HELPY	Q8gjz0 helicobacte
18	820	62.4	166	2	Q8GK49_HELPY	Q8gk49 helicobacte
19	819	62.3	166	2	Q8GJZ4_HELPY	Q8gjz4 helicobacte
20	818	62.2	166	2	Q8GK46_HELPY	Q8gk46 helicobacte
21	817	62.1	166	2	Q8GJZ9_HELPY	Q8gjz9 helicobacte
22	817	62.1	166	2	Q8GK04_HELPY	Q8gk04 helicobacte
23	816	62.1	166	2	Q8GJZ5_HELPY	Q8gjz5 helicobacte
24	816	62.1	166	2	Q8GK01_HELPY	Q8gk01 helicobacte
25	814	61.9	166	2	Q8GJY5_HELPY	Q8gjy5 helicobacte
26	814	61.9	166	2	Q8GK32_HELPY	Q8gk32 helicobacte
27	813	61.8	166	2	Q8GJY2_HELPY	Q8gjy2 helicobacte
28	812	61.7	166	2	Q8GJY1_HELPY	Q8gjy1 helicobacte
29	812	61.7	166	2	Q8GJZ1_HELPY	Q8gjz1 helicobacte
30	812	61.7	166	2	Q8GK37_HELPY	Q8gk37 helicobacte
31	812	61.7	166	2	Q8GK51_HELPY	Q8gk51 helicobacte
32	811	61.7	166	2	Q8GK14_HELPY	Q8gk14 helicobacte
33	810	61.6	166	2	Q8GK53_HELPY	Q8gk53 helicobacte
34	809	61.5	166	2	Q8GJY3_HELPY	Q8gjy3 helicobacte
35	809	61.5	166	2	Q8GJZ8_HELPY	Q8gjz8 helicobacte
36	809	61.5	166	2	Q8GK00_HELPY	Q8gk00 helicobacte
37	809	61.5	166	2	Q8GK39_HELPY	Q8gk39 helicobacte
38	807	61.4	166	2	Q8GK03_HELPY	Q8gk03 helicobacte
39	806	61.3	166	2	Q8GK22_HELPY	Q8gk22 helicobacte
40	806	61.3	166	2	Q8GK35_HELPY	Q8gk35 helicobacte
41	806	61.3	166	2	Q8GK44_HELPY	Q8gk44 helicobacte
42	805	61.2	166	2	Q8G920_HELPY	Q8g920 helicobacte
43	805	61.2	166	2	Q8GK43_HELPY	Q8gk43 helicobacte
44	804	61.1	166	2	Q8GJY4_HELPY	Q8gjy4 helicobacte
45	804	61.1	166	2	Q8GK45_HELPY	Q8gk45 helicobacte

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OM protein - protein search, using sw model

Run on: February 9, 2006, 12:01:04 ; Search time 43 Seconds
 (without alignments)
 570.588 Million cell updates/sec

Title: US-10-729-571B-2
 Perfect score: 1315
 Sequence: 1 MKIGVFD SGVGGF SVLKSL L.....FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	1315	100.0	255	2	C71924	glutamate racemase
2	1248	94.9	255	1	E64588	glutamate racemase
3	663	50.4	250	2	B81262	glutamate racemase
4	429.5	32.7	254	2	B70329	glutamate racemase
5	360	27.4	266	2	B89886	glutamate racemase
6	345	26.2	272	2	B69688	glutamate racemase
7	340.5	25.9	270	2	C81196	glutamate racemase
8	338.5	25.7	266	2	AG1582	glutamate racemase
9	334.5	25.4	266	2	AE1229	glutamate racemase
10	334	25.4	272	2	JC5587	glutamate racemase
11	329	25.0	279	1	S74824	glutamate racemase
12	326	24.8	268	1	A49473	glutamate racemase
13	317	24.1	292	2	AF1818	glutamate racemase

14	312	23.7	264	2	F98083	glutamate racemase
15	312	23.7	264	2	H95219	glutamate racemase
16	309	23.5	271	2	B86785	glutamate racemase
17	298.5	22.7	272	1	S72790	glutamate racemase
18	295.5	22.5	265	2	C69978	glutamate racemase
19	293	22.3	256	2	E97299	probable glutamate
20	288.5	21.9	271	2	F70771	probable glutamate
21	278	21.1	276	1	JC4005	glutamate racemase
22	274.5	20.9	200	2	G84033	glutamate racemase
23	274.5	20.9	369	2	C75378	glutamate racemase
24	250	19.0	287	2	AC0476	probable glutamate
25	234	17.8	262	2	F84994	glutamate racemase
26	233.5	17.8	289	2	E87708	glutamate racemase
27	233	17.7	265	2	G83062	glutamate racemase
28	227	17.3	265	2	C82358	glutamate racemase
29	220	16.7	260	2	AI0934	glutamate racemase
30	212	16.1	277	2	AE3351	glutamate racemase
31	205	15.6	289	2	I41187	glutamate racemase
32	205	15.6	289	2	B91241	glutamate racemase
33	205	15.6	289	2	G86088	glutamate racemase
34	201.5	15.3	269	2	T09430	probable glutamate
35	173.5	13.2	273	2	AI2805	glutamate racemase
36	173.5	13.2	273	2	H97584	glutamate racemase
37	171	13.0	261	2	D70112	glutamate racemase
38	142	10.8	268	2	E71329	probable glutamate
39	116.5	8.9	243	2	S16175	aspartate racemase
40	112.5	8.6	240	2	B86903	aspartate racemase
41	112	8.5	235	2	AI0867	conserved hypothet
42	110	8.4	225	2	E69427	aspartate racemase
43	109.5	8.3	232	2	B75157	aspartate racemase
44	105	8.0	226	2	H71181	probable aspartate
45	105	8.0	228	2	G71112	probable aspartate

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OM protein - protein search, using sw model

Run on: February 9, 2006, 12:06:04 ; Search time 173 Seconds
(without alignments)
615.876 Million cell updates/sec

Title: US-10-729-571B-2
Perfect score: 1315
Sequence: 1 MKIGVFD SGVGGFSVLKSL.....FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1315	100.0	255	4	US-10-335-977-7635	Sequence 7635, Ap
2	1315	100.0	255	5	US-10-729-571B-2	Sequence 2, Appli
3	1257	95.6	255	5	US-10-729-571B-4	Sequence 4, Appli
4	1248	94.9	255	3	US-09-815-242-11335	Sequence 11335, A
5	1248	94.9	255	4	US-10-282-122A-58730	Sequence 58730, A
6	1248	94.9	255	5	US-10-729-571B-20	Sequence 20, Appl
7	1248	94.9	255	5	US-10-729-571B-34	Sequence 34, Appl
8	1246	94.8	255	5	US-10-729-571B-22	Sequence 22, Appl
9	1240	94.3	255	5	US-10-729-571B-28	Sequence 28, Appl
10	1237	94.1	255	5	US-10-729-571B-6	Sequence 6, Appli
11	1237	94.1	255	5	US-10-729-571B-24	Sequence 24, Appl

12	1233	93.8	255	5	US-10-729-571B-26	Sequence 26, Appl
13	1233	93.8	255	5	US-10-729-571B-30	Sequence 30, Appl
14	1230	93.5	255	5	US-10-729-571B-18	Sequence 18, Appl
15	1229	93.5	255	5	US-10-729-571B-32	Sequence 32, Appl
16	1228	93.4	255	5	US-10-729-571B-10	Sequence 10, Appl
17	1227	93.3	255	5	US-10-729-571B-14	Sequence 14, Appl
18	1222	92.9	255	5	US-10-729-571B-16	Sequence 16, Appl
19	1204	91.6	249	5	US-10-729-571B-12	Sequence 12, Appl
20	1195	90.9	249	5	US-10-729-571B-8	Sequence 8, Appli
21	1107	84.2	219	4	US-10-335-977-7634	Sequence 7634, Ap
22	868	66.0	169	4	US-10-335-977-7633	Sequence 7633, Ap
23	663	50.4	250	4	US-10-282-122A-54641	Sequence 54641, A
24	427	32.5	262	5	US-10-729-571B-74	Sequence 74, Appl
25	373	28.4	266	4	US-10-282-122A-71383	Sequence 71383, A
26	362	27.5	267	4	US-10-282-122A-70708	Sequence 70708, A
27	361	27.5	256	3	US-09-815-242-4965	Sequence 4965, Ap
28	361	27.5	273	5	US-10-729-571B-44	Sequence 44, Appl
29	361	27.5	275	3	US-09-815-242-10720	Sequence 10720, A
30	360	27.4	266	3	US-09-815-242-5346	Sequence 5346, Ap
31	360	27.4	266	3	US-09-815-242-12340	Sequence 12340, A
32	360	27.4	266	3	US-09-815-242-12989	Sequence 12989, A
33	360	27.4	266	4	US-10-282-122A-43759	Sequence 43759, A
34	360	27.4	266	5	US-10-857-625-610	Sequence 610, App
35	360	27.4	269	4	US-10-724-972A-5578	Sequence 5578, Ap
36	355	27.0	273	5	US-10-953-901-239	Sequence 239, App
37	355	27.0	273	5	US-10-953-901-241	Sequence 241, App
38	355	27.0	275	4	US-10-282-122A-42531	Sequence 42531, A
39	354	26.9	266	5	US-10-729-571B-46	Sequence 46, Appl
40	349	26.5	268	4	US-10-282-122A-53098	Sequence 53098, A
41	340.5	25.9	270	4	US-10-282-122A-66051	Sequence 66051, A
42	339	25.8	273	5	US-10-729-571B-48	Sequence 48, Appl
43	339	25.8	277	4	US-10-282-122A-57733	Sequence 57733, A
44	337.5	25.7	264	4	US-10-282-122A-72166	Sequence 72166, A
45	334.5	25.4	266	4	US-10-282-122A-60738	Sequence 60738, A

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OM protein - protein search, using sw model

Run on: February 9, 2006, 11:57:15 ; Search time 203 Seconds
 (without alignments)
 551.929 Million cell updates/sec

Title: US-10-729-571B-2
 Perfect score: 1315
 Sequence: 1 MKIGVFD SGVGGF SVLKSL.....FHASGDVIWLERQAKEWLKL 255

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1315	100.0	255	8	ADR04138	Adr04138 Helicobac
2	1257	95.6	255	8	ADR04140	Adr04140 Helicobac
3	1248	94.9	255	4	AAU35742	Aau35742 Helicobac
4	1248	94.9	255	6	ABU30806	Abu30806 Protein e
5	1248	94.9	255	8	ADR04156	Adr04156 Helicobac
6	1248	94.9	255	8	ADR04170	Adr04170 Helicobac
7	1246	94.8	255	8	ADR04158	Adr04158 Helicobac
8	1240	94.3	255	8	ADR04164	Adr04164 Helicobac

9	1237	94.1	255	8	ADR04142	Adr04142	Helicobac
10	1237	94.1	255	8	ADR04160	Adr04160	Helicobac
11	1233	93.8	255	8	ADR04162	Adr04162	Helicobac
12	1233	93.8	255	8	ADR04166	Adr04166	Helicobac
13	1230	93.5	255	8	ADR04154	Adr04154	Helicobac
14	1229	93.5	255	8	ADR04168	Adr04168	Helicobac
15	1228	93.4	255	8	ADR04146	Adr04146	Helicobac
16	1227	93.3	255	8	ADR04150	Adr04150	Helicobac
17	1222	92.9	255	8	ADR04152	Adr04152	Helicobac
18	1204	91.6	249	8	ADR04148	Adr04148	Helicobac
19	1195	90.9	249	8	ADR04144	Adr04144	Helicobac
20	1107	84.2	219	2	AAW20880	Aaw20880	H. pylori
21	868	66.0	169	2	AAW20384	Aaw20384	H. pylori
22	843	64.1	178	2	AAW06950	Aaw06950	CagI locu
23	663	50.4	250	6	ABU26717	Abu26717	Protein e
24	427	32.5	262	8	ADR04210	Adr04210	A pyrophi
25	406	30.9	254	4	AAM48437	Aam48437	Heat-resi
26	373	28.4	266	6	ABU43459	Abu43459	Protein e
27	362	27.5	267	6	ABU42784	Abu42784	Protein e
28	361	27.5	256	4	AAU33469	Aau33469	Enterococ
29	361	27.5	273	8	ADR04180	Adr04180	E faecali
30	361	27.5	275	4	AAU35127	Aau35127	Enterococ
31	360	27.4	266	4	AAU36747	Aau36747	Staphyloc
32	360	27.4	266	4	AAU33850	Aau33850	Staphyloc
33	360	27.4	266	4	AAU37396	Aau37396	Staphyloc
34	360	27.4	266	6	ABU15835	Abu15835	Protein e
35	360	27.4	266	6	ABM71321	Abm71321	Staphyloc
36	360	27.4	266	9	ADW94670	Adw94670	Prolifera
37	360	27.4	269	5	ABP39008	Abp39008	Staphyloc
38	360	27.4	269	8	ADS06283	Ads06283	Staphyloc
39	355	27.0	273	8	ADH97048	Adh97048	E. faecal
40	355	27.0	273	8	ADH97050	Adh97050	E. faecal
41	355	27.0	273	9	AEC13405	Aec13405	Enterococ
42	355	27.0	273	9	AEC13403	Aec13403	Enterococ
43	355	27.0	275	6	ABU14607	Abu14607	Protein e
44	354	26.9	266	8	ADR04182	Adr04182	S aureus
45	353.5	26.9	264	3	AAU77700	Aau77700	Heat resi